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MYOCARDIAL ISCHEMIA AND INFARCTION

PLASMA AND TISSUE METABOLOMIC PROFILING IN A PORCINE ISCHEMIA-REPERFUSION MODEL REVEALS NOVEL EARLY MARKERS OF MYOCARDIAL INJURY

ACC Poster Contributions

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Session Title: Risk Prediction in Myocardial Ischemia/Infarction

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Background: The plasma metabolome may be an accessible reporter of the tissue metabolome, allowing earlier detection of ischemic myonecrosis than traditional biomarkers. We examined plasma and tissue metabolomic profiles in an ischemia-reperfusion animal model.

Methods: Seven swine underwent 45 min of left anterior descending artery balloon occlusion. Peripheral venous blood was collected before balloon inflation (time 0), at balloon deflation (45 min), and 90 and 180 min. Infarcted and noninfarcted tissue was obtained at 180 min. Plasma troponin (Tn) was measured at all time points. Tandem mass spectrometry (MS/MS) quantified 60 acylcarnitines and amino acids in tissue and plasma. We compared mean (SD) metabolite values in plasma between time points and between plasma and infarcted and noninfarcted tissue at 180 min.

Results: Histology confirmed myocardial infarction (MI) in all animals. Levels of many metabolites, which represent mitochondrial function, were lower in infarcted vs noninfarcted tissue (Figure, all $P < 0.05$). In corresponding 180 min plasma samples, most of these metabolites were increased from time 0 ($P < 0.05$). Similar elevations were already present at 45 and 90 min. Mean Tn levels were not significantly changed from time 0 at any time point.

Conclusion: Circulating metabolite patterns correlate with pathological evidence and tissue metabolite profiles of MI in an animal model. Further study in human subjects may elucidate a role for plasma metabolite profiles in early MI diagnosis.

Levels of amino acids (left) and acylcarnitines (right) and in infarcted vs noninfarcted myocardium

